2D Mapping of pathological nuclei

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I. Introduction

The dynamics of genome regions are associated to the functional or dysfunctional behaviour of the human cell. In order to study these dynamics it is necessary to remove perturbations coming from movement and deformation of the nucleus, i.e. the container holding the genome. In literature models have been proposed to cope with the transformations corresponding to nuclear dynamics of healthy cells. However for pathological cells such as cancer cells, the nucleus deforms in an apparently random way, making the use of such models a non trivial task. In this paper we propose a mapping of the cell nucleus which is based on the minimization of telomere motion, i.e. the motion of the very ends of chromosomes.

II. How to use the style files

Polyharmonic spline interpolation is commonly used for non-rigid registration of biomedical images [1], i.e. a point $\mathbf{p_t} = (\mathbf{x}, \mathbf{y})$ at time frame t is mapped to:

$$M(\mathbf{p_t}) = \mathbf{a} + \mathbf{a_x x} + \mathbf{a_y y} + \sum_{\mathbf{j=1}}^{\mathbf{N}} \mathbf{w_j} \|\mathbf{p_t} - \mathbf{c_t(j)}\| \tag{1}$$

where a, a_x, a_y and $\mathbf{w_j}$ are a set of weighting coefficients. These coefficients are calculated in such a way that a set of control points, $\mathbf{c_t(j)}$, are mapped to their counter points in the next time frame. It is however not always possible to find stable landmarks in this type of microscopic images. The only strong stable feature is the contour: points lying on the contour, should be mapped to other contour points to the contour. Although it is still necessary to find a mapping between contour points, i.e.

Figure 1. Two examples: in red and blue the contours and telomeres of consecutive time frames, in green the mapped telomeres.

$$\mathbf{c_{t+1}(s)} = \mathbf{M}(\mathbf{c_t}(\gamma(\mathbf{s}))) \tag{2}$$

where $c(.)$ is a parameterization of the contour and γ is a warping function. In this work, we propose to find a contour mapping based on minimizing telomere motion. Telomere motion is generally restricted to the motion induced by nuclear deformation. There might be a small displacement due to telomere dynamics, but this displacement is neglectable compared to overall motion. So the warping function in eq. (2) is optimized such that $\sum_{i=1} \|\mathbf{t_i} - \mathbf{M}(\mathbf{t_i})\|$ is minimal, where $\mathbf{t_i}$ are the telomeres centroids.

III. Conclusions

A new nucleus mapping algorithm is proposed. The proposed method does not put constraints on the possible shapes nor on the possible deformations, making this method suited for the analysis of pathological nuclei.

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References

[1] J. De Vylder, K. Douterloigne,W. De Vos, W. Philips, *2D Mapping of Strongly Deformed Cell Nuclei Based on Contour Warping* , proceedings of EMBC 2010.